Amendments to the Specification:

Please amend the specification as follows:

Paragraph at p.31; line ~~27~~ 20 to p.32, line 2

The present invention is based on the identification of naturally-occurring DNA sequence elements encoding RNA or proteins with anti-microbial activity. Bacteriophages or phages, are viruses that infect and kill bacteria. They are natural enemies of bacteria and, over the course of evolution have perfected enzymes (products of DNA sequences) which enable them to infect a host bacteria, replicate their genetic material, usurp host metabolism, and ultimately kill their host. The scientific literature documents well the fact that many known bacteria have a large number of such bacteriophages that can infect and kill them (for example, see the ATCC bacteriophage collection at ~~http://www.atcc.org~~ the Web site where the remainder of the address is atcc.org) (Ackermann and DuBow, 1987). Although we know that many bacteriophages encode proteins which can significantly alter their host's metabolism, determination of the killing potential of a given bacteriophage gene product can only be assessed by expressing the gene product in the target bacterial strain.

Paragraph at p.59, lines 7-15

A software program was developed and used on the assembled sequence of bacteriophage 44AHJD to identify all putative ORFs larger than 33 codons. Other ORF identification software can also be utilized, preferably programs which allow alternative start codons. The software scans the primary nucleotide sequence starting at nucleotide #1 for an appropriate start codon. Three possible selections can be made for defining the nature of the start codon; I) selection of ATG, II) selection of ATG or GTG, and III) selection of either ATG, GTG, TTG, CTG, ATT, ATC, and ATA. This latter initiation codon set corresponds to the one reported by the NCBI

(~~http://www.~~ Web site where the remainder of the address is ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c) for the bacterial genetic code.

Paragraph at p.59, line 23 to p.60, line 8:

Sequence homology (BLAST) searches for each ORF are then carried out using an implementation of BLAST programs, although any of a variety of different sequence comparison and matching programs can be utilized as known to those skilled in the art. Downloaded public databases used for sequence analysis include:

i) non-redundant GenBank (ftp site with the remainder of the address being ~~:~~//ncbi.nlm.nih.gov/blast/db/nr.Z),

ii) Swissprot (ftp site with the remainder of the address being ~~:~~//ncbi.nlm.nih.gov/blast/db/swissprot.Z);

iii) vector (ftp site with the remainder of the address being ~~:~~//ncbi.nlm.nih.gov/blast/db/vector.Z);

iv) pdbaa databases (ftp site with the remainder of the address being ~~:~~// ncbi.nlm.nih.gov/blast/db/pdbaa.Z);

v) *Staphylococcus aureus* NCTC 8325 (ftp site with the remainder of the address being ~~:~~//ftp.genome.ou.edu/pub/staph/staph-1k.fa);

vi) *Streptococcus pyogenes* [streptococcus pyogenes] (ftp site with the remainder of the address being ~~:~~//ftp.genome.ou.edu/pub/strep/strep-1k.fa);

vii) *S~~s~~treptococcus pneumoniae* (ftp site with the remainder of the address being ~~:~~//ftp.tigr.org/pub/data/s_pneumoniae/gsp.contigs.112197.Z);

viii) *M~~m~~ycobacterium tuberculosis* CSU#9 (ftp site with the remainder of the address being ~~:~~//ftp.tigr.org/pub/data/m_tuberculosis/TB_091097.Z) and

ix) *P~~p~~seudomonas aeruginosa* (~~http://www.~~ world wide web site with the remainder of the address being genome.washington.edu/pseudo/data.html).

Paragraph at p.72, lines 6-13

ICS biosensors have been described by AMBRI (Australian Membrane Biotechnology Research Institute; ~~http//www.~~ Web site where the remainder of the address is ambri.com.au/). In this technology, the self-association of macromolecules such as dnaN, or a fragment of dnaN, and bacteriophage 44AHJD ORF 25, is coupled to the closing of gramacidin-facilitated ion channels in suspended membrane bilayers and hence to a measurable change in the admittance (similar to impedence) of the biosensor. This approach is linear over six order of magnitude of admittance change and is ideally suited for large scale, high through-put screening of small molecule combinatorial libraries.

Paragraph at p.75, lines 11-21

The candidate protein, PT48 was excised from the SDS-PAGE gels and prepared for tryptic peptide mass determination by MALDI-ToF mass spectrometry (Qin, J., Fenyo, D., Zhao, Y., Hall, W.W., Chao, D.M., Wilson, C.J., Young, R.A. and Chait, B.T. (1997) Anal. Chem. 69, 3995-4001). High quality mass spectra were obtained (Figure 8). The PT48 proteins observed in two affinity chromatography experiments were identical as determined by the masses of the tryptic peptides. Computational analysis (~~http://~~ http site where the remainder of the address is prowl.rockfeller.edu/cgi-bin/ProFound) of the mass spectrum obtained identifies the corresponding ORF in the *S. aureus* nucleotide sequence in the University of Oklahoma *S. aureus* genomic database (~~http://www.~~ Web site where the remainder of the address is genome.ou.edu/staph.html). The identity of that protein which binds specifically to GST ORF25 is the DNA-directed DNA polymerase III beta subunit (Genbank accession #1084187) (Figure 9 and Figure 10).